

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: August 13, 2001, 09:44:54 ; Search time 3626.83 Seconds  
(without alignments)  
11766.617 Million cell updates/sec

Title: US-09-784-340-1  
Perfect score: 2759

Sequence: 1 caaccatgcagcatcagtglt.....ctgtcagccgttactgtagcg 2759

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1344157 seqs, 7733874588 residues

Total number of hits satisfying chosen parameters: 2688314

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

- 1: gb\_ba1.\*
- 2: gb\_ba2.\*
- 3: gb\_ba3.\*
- 4: gb\_in1.\*
- 5: gb\_in2.\*
- 6: gb\_in3.\*
- 7: gb\_om.\*
- 8: gb\_ov.\*
- 9: gb\_pat1.\*
- 10: gb\_pat2.\*
- 11: gb\_ph.\*
- 12: gb\_pl1.\*
- 13: gb\_pl2.\*
- 14: gb\_pl3.\*
- 15: gb\_pl4.\*
- 16: em\_ba1.\*
- 17: em\_ba2.\*
- 18: em\_fun.\*
- 19: em\_hugo\_hum.\*
- 20: em\_hugo\_inv.\*
- 21: em\_hugo\_rod.\*
- 22: em\_hug\_hum1.\*
- 23: em\_hug\_hum2.\*
- 24: em\_hug\_hum3.\*
- 25: em\_hug\_hum4.\*
- 26: em\_hug\_hum5.\*
- 27: em\_hug\_hum6.\*
- 28: em\_hug\_hum7.\*
- 29: em\_hug\_hum8.\*
- 30: em\_hug\_inv1.\*
- 31: em\_hug\_inv2.\*
- 32: em\_hug\_other.\*
- 33: em\_hug\_rod.\*
- 34: em\_hum1.\*
- 35: em\_hum2.\*
- 36: em\_hum3.\*
- 37: em\_hum4.\*
- 38: em\_hum5.\*
- 39: em\_hum6.\*
- 40: em\_hum7.\*
- 41: em\_in.\*
- 42: em\_om.\*
- 43: em\_or.\*

- 44: em\_ov.\*
- 45: em\_pat.\*
- 46: em\_ph.\*
- 47: em\_pl.\*
- 48: em\_ro.\*
- 49: em\_sts.\*
- 50: em\_sy.\*
- 51: em\_un.\*
- 52: em\_v1.\*
- 53: gb\_sts1.\*
- 54: gb\_sts2.\*
- 55: gb\_sts3.\*
- 56: gb\_sy.\*
- 57: gb\_un.\*
- 58: gb\_v11.\*
- 59: gb\_v12.\*
- 60: gb\_hug1.\*
- 61: gb\_hug2.\*
- 62: gb\_hug3.\*
- 63: gb\_hug4.\*
- 64: gb\_hug5.\*
- 65: gb\_hug6.\*
- 66: gb\_hug7.\*
- 67: gb\_hug8.\*
- 68: gb\_hug9.\*
- 69: gb\_hug10.\*
- 70: gb\_hug11.\*
- 71: gb\_hug12.\*
- 72: gb\_hug13.\*
- 73: gb\_hug14.\*
- 74: gb\_hug15.\*
- 75: gb\_hug16.\*
- 76: gb\_hug17.\*
- 77: gb\_hug18.\*
- 78: gb\_hug19.\*
- 79: gb\_hug20.\*
- 80: gb\_hug21.\*
- 81: gb\_hug22.\*
- 82: gb\_hug23.\*
- 83: gb\_hug24.\*
- 84: gb\_hug25.\*
- 85: gb\_pr1.\*
- 86: gb\_pr2.\*
- 87: gb\_pr3.\*
- 88: gb\_pr4.\*
- 89: gb\_pr5.\*
- 90: gb\_pr6.\*
- 91: gb\_pr7.\*
- 92: gb\_pr8.\*
- 93: gb\_pr9.\*
- 94: gb\_ro1.\*
- 95: gb\_ro2.\*
- 96: gb\_in4.\*
- 97: gb\_pr10.\*
- 98: em\_ba3.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2130.6	77.2	2786	89	AK025587 Homo sapi
2	1038.8	37.7	2547	94	AF175221 Cavia por
3	994.8	36.1	212904	66	AC021146 Homo sapi
4	967.4	35.1	1650	9	AX040087 Sequence
5	952.4	34.5	13865	72	AC055794 Homo sapi
6	821.2	29.8	1766	93	HS46054 Homo sapi
7	782	28.3	2090	97	HSU08854 Human UDP g
8	778.8	28.2	2114	89	AF180322 Homo sapi



QY	802	aalacgaacatalatgggattlignaalttcctcaacatataccaaacttaactltagtltgt	861
Db	601	AATACGAACATATTTGGATTTTGAATTTCCCTCAACCATACCAACCTTAATTGATTTGT	660
QY	862	tggagatctgcactgtaaacctgccaagcttggcctaagaaatggaatattgtcca	921
Db	661	TGGAGGATTTGCACCTGTAAACCTCCCAAGGCTTTGGCTTAAAGAAATGGAAAAATTTTGTCCA	720
QY	922	gagcttaagggaagaatgagatgtattgtgttttcttcggggtaactgtttcaaaatgtac	981
Db	721	GAGTTTACGGGAGAGATGTAATTTGTGTGTTTCTCTGGGGTCACTGTTTCAAAATGTTAC	780
QY	982	agaagaanaagcctaataatcaltgcttcagcccttgcccaatcccaagaagtgltatg	1041
Db	781	AGAGAGAAAAGGCTAATATCATCTTCCTTCAGGCCCTTGGCCCAATCCACAGAAAGTGTTATG	840
QY	1042	gaggtcaaaagaaaaaaacatcacataggagccaatactcgtgctatgattgat	1101
Db	841	GAGGTCAAAAGGAAAAAAACCATCCACATTAGAGGCCAATACTCGCGCTGTATGATTGAT	900
QY	1102	accocgaatgattcttccttggtatccccaaccaaagcctttatacctaagtgtaat	1161
Db	901	ACCCCAAGATGATCTTCTTGCTATCCCAAAACCAAGCTTTATCATCTATGTTGAAT	960
QY	1162	gaatggatctatgaagcatattaccatggggtcccatggtggaggtcccatattgg	1221
Db	961	GAAATGGATCTATGAAGCTATTTACCATGGGGTCCCTATGTGTGGAGTTCCCATATTTGG	1020
QY	1222	tgatcagcttgataacatagctcacatgaagagccaaagagcagctgtagaanaaact	1281
Db	1021	TGATCAGCTTGAATACATAGACTCACATGAAGGCCAAAGAGCAGCTGTAGAAATTAACCT	1080
QY	1282	caaaactatgacaagcgaagaatttaactgaggcttggagaaacgtcaatccgattcctc	1341
Db	1081	CAAAACTATGACAAAGGAAGATTTAAGAGGGCTTTGAGAAACGTACTTAACCGATTCTC	1140
QY	1342	tataaagaagaatgcatagatatacoaagaattcaacatgataacactgtaaagccct	1401
Db	1141	TATATAAGAAATGCTATGATGATTAATCAAGAAATTCACCATGATCAACCTGTAAAGCCCT	1200
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Db	1201	AGATCAGAGAGTCTTCTCGATCGAGTTTGTCAATGCGCCACAAAGAGCAACCTGCG	1260
QY	1462	atcagctgcccatgactcaaccgtgtccagcaactactctatagatgtgattgggtcct	1521
Db	1261	ATCAGCTGCCCAAGACCTCACCTGGGTCCAGCACTACTCTATAGATGTGATGGGTCTCT	1320
QY	1522	gctgacctgtgtggcaacgctatcttctgttccaaaaatgthtttatttcctgtca	1581
Db	1321	GCTGGCCTGTGTGGCAACGCTAATATCTTGTTCACAAAATGTTTTATTTTTCCTGTCA	1380
QY	1582	aaaatttaataaacatagaaaagatagaagagggaaatagatcttccaaatlcagaanaa	1641
Db	1381	AAAATTTAATAAATAGAAAAGATAGAAAAGAGGAATAGATCTTCCAAATTCAGAAA	1440
QY	1642	gacctgaatggggtatccctggttaattccagccacatagaattgggtgaaaaactgtcat	1701
Db	1441	GACCTATGGGGTAAATTCCTGTTAATTTCCACGCCACATAGAAATTTGGTCAAAAACCTTGCTAT	1500
QY	1702	tttccatatatcatctctgttatatttatcttgaactatagatagccatagaaatccatgacat	1761
Db	1501	TTTTCAATATATCTAATTCGTATTATTTTATCTTAGCTAATATAGCCTAGAAATTCACAGATCAT	1560
QY	1762	gaagttgtgagtaatactcaatcttctcgttgacaatttcctagggtgtactactcctct	1821
Db	1561	GAGGTTGTGAGTATATCTATCTCTTTCGTTGTAATTTCCTAGAGGTCTTAACTCTCTTCT	1620
QY	1822	ctcaactttgtacacaagaagcatgaaataactaaatttccctatttcgtatatcaactgt	1881
Db	1621	CTCACCTTTGTGACACAGGACATGAAATACATCTCAAAATTTTCCATATTTCTCATATAGACTGT	1680

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QY	1942	ccttgatgcttgacaacaacgatggatgataagaagataaaatgtaaattccaanaatt	2001
Db	1741	CCTGGTGTCGGCCCAACACATGGATATTAAGAGGTAAACACTTAAATTCACAAAATT	1800
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QY	2062	tgattttctttccaattaalaagacccttcatacacccagcatctactgctcaga	2121
Db	1861	TGATGTTTTCTTTTCAATTAATAATAAGCCTTCTACATACCAGCATCAGTAGATCTCAGA	1920
QY	2122	caatgaatttgtcaaaaatgaacgataggcgatctacactcagaatagtttgtatattcca	2181
Db	1921	AAATAAATTTGCTAATATATGATGACATGCGATTTATGCTTAAGAAAAAGTTTGCTGATTTTCCA	1980
QY	2182	catcctcaatcagatgctgatagccfacaattctgccatcacttaactgaca-ttttttg	2240
Db	1981	TGACCTCATCTAGATGTCATGCGCTACATTTCTGCCATATACTCACCAAATACTTTTTC	2040
QY	2241	tgtgtctctgatagataaatagacagcttctctattctatgtgcccaataataaagaacgt	2300
Db	2041	TGTTTTCTTGATGATATAAAGACCTTTCATGATGATTGCCATCAAAATPACAAAGAACTA	2100
QY	2301	aaat-ttcttacaatagagaaaaatgcccataagaatalccaagttaaagagalia-ctttg	2358
Db	2101	TTTTTTTTTCTCCATATGACACACATGTCAGTAAGATATPACAAAGGTGAACAGATTAATTTTGG	2160
QY	2359	agataagatcacatagaanaatagtatgtatgtatcttgattttaanaaatttaattga	2418
Db	2161	GGAATTAAGTACATTTTGAATATATGTGTGTAATTAATCTGAGTTATATAAA-TTTATTGGA	2219
QY	2419	tagtacacct-----gattlaaatgtcatactttt-aaaatgatgataactcataatc	2471
Db	2220	TAGTNACACTTAAGAAGATTTTATATGTTTATCTTTTAAAAATGATGAATCTCATTAATTC	2279
QY	2472	ttatctctaatcaaaagtataattactgttagaaaaataaagaagatgctgtttctgaa	2531
Db	2280	TTATCTCTTAAATCAAAAGATATTAATTACTGTGAGAAAAATAAAGAGATGCTGTTCGAA	2339
QY	2532	agtaaa 2538	
Db	2340	AGTAAGA 2346	
RESULT 2			
AF175221	2547 bp	mRNA	ROD 29-AUG-1999
LOCUS	Cavia porcellus UDP glucuronosyltransferase UGT2A3 mRNA, complete cds.		
DEFINITION			
ACCESSION	AF175221		
VERSION	AF175221.1	GI:5802603	
KEYWORDS			
SOURCE	domestic guinea pig.		
ORGANISM	Cavia porcellus		
REFERENCE	Eukaryota; Metazoa; Chordata; Granulata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Rodentia; Hystriocognathi; Cavillidae; Cavia.		
TITLE	1 (bases 1 to 2547)		
JOURNAL	Smith,S.A., Nagalla,S.R., Andrews,D.P. and Olsen,G.D.		
REFERENCE	Morphine regulation of a novel uridine diphosphate		
AUTHORS	glucuronosyltransferase in guinea pig pups following in utero		
TITLE	exposure		
JOURNAL	MOL. Genet. Metab. (1999) In press		
REFERENCE	2 (bases 1 to 2547)		
AUTHORS	Smith,S.A., Nagalla,S.R., Andrews,D.P. and Olsen,G.D.		
TITLE	Direct Submission		
JOURNAL	Submitted (02-Aug-1999) Pediatrics, Oregon Health Sciences		
FEATURES	University, 3181 SW Sam Jackson Park Road, Portland, OR 97201, USA		
	Location/Qualifiers		

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VAEMLGPEVNNLKFSGMHTIEKYGGLPAPSVYPRVGLITMTYEMERYKNVFS
VLPFDIOOYDKKPPDOYSEALGRPTICELMGRALITLITYDREPRRYLNEF
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BASE COUNT 765 a 469 c 523 g 790 t
ORIGIN

Query Match 37.7% Score 1038.8; DB 94; Length 2547;
Best Local Similarity 76.0%; Pred. No. 1.2e-175;
Matches 1299; Conservative 0; Mismatches 402; Indels 9; Gaps 1;

26 ggaacgcacatgatgagctctgcaagaatcagcttctgtattctctctgcaagctcttc 85
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8 GGAGAGCCAGATGGCTCTGGAGATGGCTTCGACGTCTGCTGCTGCTGCTGCTGCTG 67

86 tctgtgctgctgagctctctggaagaatccctgctgctgctgctgctgctgctgctg 145
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68 TGTGCGCGCTCTGATGATCTGTGGGAAGGTGCTGTGCTGCGGTGTAATGAGCCACTGG 127

146 cthaatgcaagctcctctgagaagaatcagctgagcagcagcagcagcagcagcagcag 205
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128 CTCATTTAAAGACTCTCTCTGAGAGCTTGTAAGAAAGAGACATGAGGATGAGGTTCTG 187

206 acccactcaagaagctcgttaattgactacagaagcctctgcaattgaaattgagctg 265
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266 gtccataatcccaagcagaagaagaataatgaata-----tttggtaacct 316
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248 ATGCCGTGACCACTGACAAAACATGCTGAGAAATATATGATGATTAAGTAAGTA 307

317 gctctgaatgctctgcaagcctcacaacctggaacagctacgtatataaatgaatttt 376
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308 GGTGTGAATGTCATGCCAACATGCTCTGTGCAATCAGGAAACTACTGCAACAACTTC 367

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368 TTTGTTCAATATCACTGAACATTTAGCTTAAGTAAGTAAGTAAGTAAGTAAGTCTCC 427

437 ctatataagaagctacagaagaacacacacacacacacacacacacacacacacacac 496
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428 CTCATGAAGAAGCTCGGAGCTCCAGTATGATGATGATGATGATGATGATGATGATGAT 487

497 tctggaagcctgagctgagctgagctgagctgagctgagctgagctgagctgagctg 556
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488 TGTGGGAGACTGTGTGCTGAGATGCTTTGGGTTCTTTGTGTAACATGCTAAAGTCTCC 547

557 gtagaagagaatataagagaagcgtgtggaagcctccacacacacacacacacacacac 616
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617 gtgcacatgacagaagcagacagaagcagcagcagcagcagcagcagcagcagcagcag 676
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608 GTTCCCTCTGGGGGACTCACAAACAGATGACATTTATGGAAGGGGTGAAGATATGCTG 667
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QY 677 cttcagatttctcactctgagctcaggaatcagactacatcatcttttggagaagatt 736
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DB 668 TTTTCAATTTTGTGACTTCTGATCCAGCATATGACTATATAGTTTGGATGCTGTTT 727

737 tatagaagcaltgaagaagccactacatlatggaagctgtggagaagctgagata 796
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DB 728 TACAGTGAAGCTTTAGGAAGACCACTACATATATGAGATATATGAGTAAAGCTGAAT 787

797 tggctatcagaacatattggagtttgaatttcctccaaacacacacacacacacacac 856
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DB 788 TGGCTATATCCGACATATCTGGATTTTGAATTTTCTGCTCCATATTTGCTAATTTTGA 847

857 ttgtctggaagctgagcagctgaacacacacacacacacacacacacacacacacacac 916
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917 gtccagaagctcaggaagagatgagctgagctgagctgagctgagctgagctgagctg 976
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DB 908 GTCCAGAGTTCAGGTGAAGATGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 967

977 gtacagaagaagaagcctaataatcattgcttgaagccttggccagatccacagaagctg 1036
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DB 1028 TTATGAGATFACAAAGGAAGAAAGCCAGCACCTTTTGAAGCCAAATCTGGCTTTGAT 1087

1097 tggatccccagaatgactctctgtgctatcccaaaacacacacacacacacacacacac 1156
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1157 ggaatgaagagcctcctatgaagctatccatgaagcctgagctgagctgagctgagctg 1216
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1217 ttgtgtagcagcttgataacacatgacatgaagcagaagcagcagcagcagcagcagcag 1276
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DB 1208 TTTTCTGATCAGCCTGACAACTCTGCTGATGAAAGCCAAAGACACCTGTGGAGTCTG 1267

1277 aactcaaacactatgacagcagaagcttactgagcagccttggagaagcagctcattaccgt 1336
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DB 1268 AACATGAACCAATGACAAAGTGCAGACCTGCTGGGCTGTGAGGACATGACATCAATGAC 1327

1337 tccctcattaaagagatgctatgagatlatcaagaatccacatgataacacagcagcag 1396
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1397 cccctagatcagagcagctctctgagcagcttgcatagcgcacaaagagcagcagcagc 1456
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1637 agaaagacacacacacacacacacacacacacacacacacacacacacacacacacac 1696
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DB 1628 TTAAGTGTGAGACTGGCTGCTCAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1687

1697 gctatttcatatcatatctcgtattt 1726
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Db	1048	ATTTCGATCGGGAATAAACCAATACTCTTATGACATCAATACCTCGGCTGTACAACTGGATACC	1107
Qy	1105	ccgaatgatctctctgtgcatcccaaaccaagctttatcatcactgagtggaatgaa	1164
Db	1108	CCAAATATGATCTTTCTGTGATCCCAAAACCAAAAGCTTTTATCATCAATGATGGAAATGAA	1167
Qy	1165	tgagatcatgaagcttattccatcgtgggtccctcattgctggtggaagttcccatattggtgta	1224
Db	1168	TGGGATCTATTAACCTATTTCACATGGGGTCCCTATGATGGGAGTTCCTCATTTTGGTGA	1227
Qy	1225	tcaagcttgataacatlagcttcacatggaagccaaaggaagcagctgtagaataaactcaa	1284
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AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
TITLE	1 (bases 1 to 138665)		
JOURNAL	Biiren, B., Linton, L., Nusbaum, C. and Lander, E.		
REFERENCE	Homo sapiens chromosome 4, clone -2005D20		
AUTHORS	Unpublished		
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	Biiren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,		
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	Boguslavsky, I., Boukhalter, B., Brown, A., Burkett, G.,		
	Campoliano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S.,		
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	Dodge, S., Domino, M., Doyle, M., Ferreira, P., Fitzhugh, W., Gage, D.,		
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TITLE
JOURNAL
COMMENT
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Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatsis,A., Klein,J., LaRocque,K., Lamazares,R., Landers,T., Lehoszky,J., Levine,R., Lien,C., Liu,G., Locke,K., MacDonald,P., Marquis,N., McCarthy,M., McEwan,P., McGovir,A., McErihan,K., McHeeters,R., McIdrum,J., Meneus,L., Mihova,T., Miranda,C., Mienga,V., Morrow,J., Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,T.M., Oliver,J., Peterson,K., Pierre,N., Pisanic,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D., Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J., Testaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zimmer,A. and Zody,M.

Direct Submission

Submitted (18-APR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
On May 14, 2000 this sequence version replaced gi:7582623.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html

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Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence.submissions@genome.wi.mit.edu

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Project Information

Center project name: L7347
Center clone name: 2005_D_20

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Summary Statistics
Sequencing vector: M13; M7815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 134168 bases at least Q40
Consensus quality: 136964 bases at least Q30
Consensus quality: 137776 bases at least Q20
Insert size: 176000; agarose-fp
Insert size: 138165; sum-of-ctrls
Quality coverage: 4.1 in Q20 bases; agarose-fp
Quality coverage: 5.2 in Q20 bases; sum-of-ctrls

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* NOTE: This is a 'working draft' sequence. It currently
* consists of 6 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

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* 1 4325: contig of 4325 bp in length
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* 4326 4425: gap of 100 bp
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* 4426 14722: contig of 10297 bp in length
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* 14723 14822: gap of 100 bp
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* 14823 30375: contig of 15533 bp in length
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* 30376 30475: gap of 100 bp
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Best Local Similarity 71.9%; Pred. No. 7.4e-137;
Matches 1107; Conservative 0; Mismatches 418; Indels 15; Gaps 2;

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VERSION U08854.1 GI:475758
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Green,M.D., Oturu,E.M., and Tepfly,T.R.
TITLE Stable expression of a human liver UDP-glucuronosyltransferase
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JOURNAL Drug Metab. Dispos. 22 (5), 799-805 (1994)
MEDLINE 95136867
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AUTHORS Green,M.D.
TITLE Direct Submission
JOURNAL Submitted (13-APR-1994) Mitchell D. Green, Department of
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RESULT 8  
AF180322

LOCUS	AF180322	2114 bp	mRNA	PRI	14-SEP-1999
DEFINITION	Homo sapiens UDP-glucuronosyltransferase 2b15 (UGT2B15) mRNA, UGT2B15-Y85 allele, complete cds.				
ACCESSION	AF180322				
VERSION	AF180322.1				
KEYWORDS	GI:5881245				
ORGANISM	human.				
REFERENCE	Homo sapiens				
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.				
TITLE	1 (bases 1 to 2114)				
JOURNAL	Lewesque, E., Beaulieu, M., Green, M.D., Tephly, T.R., Belanger, A. and Hum, D.W.				
MEDLINE	Isolation and characterization of UGT2B15(Y85): a				
REFERENCE	UDP-glucuronosyltransferase encoded by a polymorphic gene				
AUTHORS	Pharmacogenetics 7 (4), 317-325 (1997)				
TITLE	2 (bases 1 to 2114)				
JOURNAL	Lewesque, E., Beaulieu, M., Green, M.D., Tephly, T.R., Belanger, A. and Hum, D.W.				
MEDLINE	Direct Submission				
REFERENCE	Submitted (24-AUG-1999) Molecular Endocrinology, CHU Research				
AUTHORS	Center, 2705 Laurier Blvd, Ste-Foy, Quebec G1V 4G2, Canada				
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ORIGIN					
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Oy	383	gaataaagaaggaaactttaaaatgatgtctgaagactttctacatacagaagctatg	442
Db	393	GAAATTTATGACTACAGTAACAACACCTCTGTAAAGATGCACTTTTGAATTAAGAACTTATG	452
Oy	443	aagaagctacagaagaaccaactacgatgtatagcttatagaacctgtgatctccgttga	502
Db	453	ATGAACACTACAAAGGTCAAAATTTGATGTATTTCTGGCAATGCCCTTATATCCGTGGT	512
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Oy	1043	aggtacaagaagaaaaaacatccacactctgtggagcaaatatctcgtgtgatgatgatga	1102
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Query Math.	Best Local	Similarity	28.18	Score	775.6	DB	97	Length	2107
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mRNA, complete cds.  
ACCESSION AF112112  
VERSION AF112112.1 GI:4580601  
KEYWORDS crab-eating macaque.  
SOURCE Macaca fascicularis  
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Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
Cercopithecinae; Macaca.  
REFERENCE 1 (bases 1 to 2108)  
AUTHORS Belanger, G., Barbier, O., Hum, D.W. and Belanger, A.  
TITLE Molecular cloning, expression and characterization of a monkey  
steroid UDP-glucuronosyltransferase, UGT2B19, that conjugates  
testosterone  
JOURNAL Eur. J. Biochem. 260 (3), 701-708 (1999)  
MEDLINE 99203465  
REFERENCE 2 (bases 1 to 2108)  
AUTHORS Belanger, G., Barbier, O., Hum, D.W. and Belanger, A.  
TITLE Direct Submission  
JOURNAL Submitted (07-DEC-1998) Molecular Endocrinology, CHUL Research  
Center, 2705 Laurier Blvd, Sainte Foy, Quebec G1V 4G2, Canada  
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QY 985 agaaaaggtcaatatattgtctcagcccttgcacagatcccaagaagtgatagag 1044
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Oy 1585 atttaataaacctagaatagaagaagggaatagcttcttc 1628

Db 1584 GTTTTGTAGAACAGAGAAAGAGGGAAAAGATTAAATTAGCTC 1627

RESULT 13

AF184901

LOCUS AF184901

DEFINITION Mus musculus olfactory UDP glucuronosyltransferase mRNA, complete cds.

ACCESSION AF184901

VERSION AF184901.1

KEYWORDS GI:10441349

SOURCE house mouse.

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS Heydel,J.M.

TITLE Mus musculus mRNA for olfactory UDP glucuronosyltransferase

JOURNAL unpublished

REFERENCE 2 (bases 1 to 1584)

AUTHORS Heydel,J.M.

TITLE Direct Submission

JOURNAL Submitted (10-SEP-1999) Biochemistry, University, Bvd Jeanne D'Arc, Dijon 21000, France

FEATURES

Source Location/Qualifiers

1..1584

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BASE COUNT 445 a 341 c 360 g 438 t

ORIGIN

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Oy 134 atgagccattgtgcttaagtcaagatcattctagaagaagcctcatatgtagaagccatgag 193

Db 88 GGCACCTACTGGCTAAAGTTAAGATCAATTAAGATGGAACCTCTAAGAAAAGACATAT 147

Oy 194 gtaacagatattaccacacccaacagccttcgttaattgactaacagaagaagccttcctcatg 253

Db 148 GTGACTGTGCTGTGTGGCTCGCGGGCCCTTTTCATCACCACACATCCATCGCCATCTGTG 207

Oy 254 aaattgagtggttcataatgccacagagcagaacagaagaatgaaatatttctgttac 313

Db 208 ACATTGTGAATATATCCACAGTGCCTTTGGCAAGAAAAAATTGGAAGGTGATCAAAACAG 267

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QY	362	aaattaaatgcttttttttgttgaataaagaaggaaactttaaaatgctgtgaagcttt	421
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QY	422	atctcaacatcgaagccttatgaagaactcaagaagaaacacacagatgtlaatgcttata	481
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QY	482	gacctgtgaltccctgltbgaagactgtaatgctgaatgtcgtgcagtcgccctttgtgc	541
Db	448	GACCCGTGATTTTCCCTGTGGGACATGCTGGCTTTAAACTGGGAATTCATTATATCAT	507
QY	542	aaacttgaatttctctgtagagaagaaatgtagcgaagctgtgaggaaacttcagcttca	601
Db	508	TCTTTGGCGTTTTTCCCTGTCCACAGTGGAAAGCATTTGTGAAAGGTCCCATTTCCCT	567
QY	602	ctttccctatgtaactgtgcctatgacagagatacagacagaatgtaactttctggaaga	661
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QY	662	gtaaaaaatlcaatgcttcaagtttgccttccacttcgtgattcgaagtaagatacatacat	721
Db	628	GTAAGAAACCTTCATTCTTACCCGATCAGACTACATGATGTT---GAAACCTTTGGAAG	684
QY	722	ttttgggaagaagtttatagttaagaactatggaagagccactatcatatgtgaagctgtg	781
Db	685	CAGTGGGATTCCTTTATTTACTAAAGCTTTTGGAAAGCCACGACACTGTGTGAGACTATG	744
QY	782	ggaagaagcttgatagatgagcttaatacagaacatattggaatttgaatttccctcaacac	841
Db	745	GGAATAGCTGTGATTTGGCTATATGCGAAGCTATTTGGATTTTGAATTTCTCTGCTCAAT	804
QY	842	caacctaaactttgagtttgttgaagagatgtgcactgtlaaacttgcgaagctttgcttaag	901
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QY	902	gaaatggaataatttctgccagagttcaggagggaagaatggtatgtgtgttttctctggg	961
Db	865	GAAATGGAAAGTGTGTGTCACAGCTCAGGGGAAACATGATATGTGTGTTTCTGTGGGG	924
QY	962	tcaactgtttcaaaatgttatacgaagaagaagcctaatacatattgcttcagcccttgcag	1022
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QY	1022	atccccacgaagaagtgtatagaggtacaaaggaagaaacacatccacatlagagccaat	1081
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Db	1045	ACAAGACTGTTTGGATTGGATTCCTCAAAAGATCTTCTTGGATCTCCAAAACCGAGAGCT	1104
QY	1142	tttatcactatlgltbgaagaatggagatctatgaagcattatcaatgaatgggttccctatg	1201
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Db 1405 AAGAGGACCAAGACCTTGTGTGTGACGACGACGACGACGACGACGACGACGACGAC 1464  
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OY 1562 tgtttttatttctcctgcaaaatlaaataaactagaagataagaagaggaatag 1621  
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RESULT 14  
AF064200 2097 bp mRNA PRI 11-DEC-1998  
LOCUS Homo sapiens UDP-glucuronosyltransferase 2B4 precursor (UGT2B4)  
DEFINITION AF064200  
AF064200 mRNA, UGT2B4\*E458 allele, complete cds.  
ACCESSION AF064200.1 GI:3153831  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
human.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
REFERENCE  
AUTHORS  
JOURNAL  
TITLE  
2 (bases 1 to 2097)  
UDP-glucuronosyltransferase encoded by a polymorphic gene  
pharmacogenetics (1999) In press  
Levesque, E., Beaulieu, M., Hum, M. and Belanger, A.  
Submitted (08-MAY-1998) Molecular Endocrinology, CHUL Research  
Center, 2705 Laurier Blvd, Ste-Foy, PQ G1V 4G2, Canada

FEATURES  
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## CDS

BASE COUNT 653 a 393 c 435 g 616 t  
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Query Match 27.6% Score 762.8; DB 88; Length 2097;  
Best Local Similarity 68.6%; Pred. No. 1.9e-126;  
Matches 1100; Conservative 0; Mismatches 492; Indels 12; Gaps 3;

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Db 79 TAGCTTGCGAGATCTGTGGAAGGTGCTGTGGCCACAGAAATTCAGCCATGATGAA 138  
OY 151 tgaagagtcatttagaagagcctcatagtgagagagccatgagtgatgactca 210  
Db 139 TATTAAGCAATCCCTGGATGAACTTGTCCAGAGAGGTCATGAGGTGACTGTATGGCATC 198  
OY 211 ctcaagccttcgttaattgactacgaagccttcctgcatgtaattgagtgctca 270  
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OY 271 tatcccaagcagcagaagagaagaataatgaaatatttgtagcctcgtga-----a 324  
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Db	1576	GTTTGTGTAGAACAGAGAAAGGAGGAGAAAGAGATTAAATTACCTC	1619
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LOCUS	AF081793		
DEFINITION	Homo sapiens UDP glucuronosyltransferase 2B4 precursor (UGT2B4)		
ACCESSION	AF081793		
KEYWORDS	AF081793.1 GI:3426331		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
TITLE	1 (bases 1 to 2091)		
JOURNAL	Jin, C.-J., Miners, J.O., Lillywhite, K.J. and Mackenzie, P.I.		
MEDLINE	CDNA cloning and expression of two new members of the human liver		
REFERENCE	UDP-glucuronosyltransferase 2B subfamily		
AUTHORS	Biochem. Biophys. Res. Commun. 194 (1), 496-503 (1993)		
TITLE	2 (bases 1 to 2091)		
JOURNAL	Mackenzie, P.I.		
MEDLINE	Direct Submission		
REFERENCE	Submitted (30-JUL-1998) Clinical Pharmacology, Flinders University		
AUTHORS	of South Australia, Bedford Park, SA 5042, Australia		
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Query Match	27.5%; Best Local Similarity	Score 758; 68.4%;	DB 88; Pred. No. 1.3e-125;	Length 2091;
Matches 1097;	Conservative	0;	Mismatches 495;	Indels 12; Gaps 3;
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Db				
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151	tgtcaagctatcttagaagagctcatagtgagagggccatgagtgtaacagtatctactea	210		
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149	TPTAAAGACAAATCCGATGAGAACTGTCCAGAGAGGTATAGAGTGACGTATGGCATC	208		
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209	TTCAGCTTCCATTTCTTTCGATCCCAACGCGCCATCTACTCTTAAATTGAAGTTTATCC	268		
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269	TCTATCTTTAACTAANAACGAGTTTGAGGATATTTTCAACAGCGCTTGTTAAGAGATGGCC	328		
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385	aataagaggaacttcaaaaatgatatgtgtgagagcttatactacaatcgaagctatgaa	444		
Db				
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445	gaagctcaggaagaacaactacgagtataatgttataagaccttgatccctgtggaga	504		
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449	GAAACTACAGGAGTCAAGATTGATGTTGTTTTCGACAGCGTGTTTCCCTTTGGGTGA	508		
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Db				
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Db				
629	GTCAGAACTAACTGACCAATATGACTTTCTATAGAGGGGTAAAAAATATGATTTATGTGCT	688		
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Db				
689	TTATTTTGAATTTTGGTTCCAAATATTTTGACATGAAGAGTGGGATCAGTTCTACAGTGA	748		
745	ggcatatgagaagcccactacatatgtfagaagcgtgtggaaaagcttgagatagtgctaat	804		
Db				
749	ACTTCTAGAAACCCACTACTCTTATCTGAGCAATATGGCAAAAGCTGCATATGTGCTTAT	808		
805	acgaacatatttgagtttgaatttccccaacactacacaaacttaactgaattgtgttg	864		
Db				
809	TGCAGACTRACGTGGATTTTTCATTTTCTCCACCCACTCTTTACCAAAATGTTGAGCTTGCG	868		
865	aggatttgcactgtlaaacctgtccaagctttgtcctaaggaatagtgaanaatttgtlccagag	924		

